b) a naturally-occurring human polynucleotide sequence variant encoding an amino acid sequence having at least 90% sequence identity to the sequence of SEQ ID NO:1 and

c) a polynucleotide sequence complementary to a) or b).

20. (Reiterated) A method of detecting a target polynucleotide in a sample, said target polynucleotide having the sequence of a polynucleotide of claim 19, comprising

hybridizing the sample with a probe comprising at least 15 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and

detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

21. (Reiterated) A method of claim 20, wherein the probe comprises at least 30 contiguous nucleotides.

22. (Reiterated) A method of claim 20, wherein the probe comprises at least 60 contiguous nucleotides.

REMARKS

Claims 1, 18-22 are pending in this divisional application. Claim 1 was withdrawn from consideration pursuant to a restriction requirement. Claim 17 was canceled. Applicants reserve the right to prosecute the non-elected and the canceled claims in subsequent divisional applications.

Claims 18-22 are currently being examined on merits. Claim 19 has been amended by entry of these amendments to further clarify the invention. Support for the amendments can be found in the specification, and in the claims as originally filed. No new matter is added by any of these amendments. Entry of these amendments is respectfully requested.